Amendments to the Specification

Please replace the paragraph on page 4, lines 19-23, with the following rewritten paragraph:

--According to yet another aspect of the invention, isolated nucleic acid molecules and amino acid molecules are provided that have, by way of example, at least 15, 20, 30, 40, or 50 contiguous nucleotides or amino acid residues with the sequences shown in SEQ ID NOS: 1, 4, and 17; or the complementary strands ~~thereorof~~ thereof, or SEQ ID NOS: 3, 6, or 18, respectively.--

Please replace the two paragraphs beginning on page 33, line 5, with the following rewritten paragraphs:

--Identification of *A. nidulans* α-1,2-mannosidase 1C: A second lambda clone containing the full length α-1,2-mannosidase 1C gene was recovered and two non-overlapping *Bam*HI subclones (4 kb and 6 kb) were isolated, which together contained the gene and flanking regions. Again, the sequence across the *Bam*H1 subcloning junction was verified to eliminate the ~~possiblity~~ possibility of missing sequence. The gene and several hundred bp of flanking region were fully sequenced (Accession #: AF233287).

Example 6

~~Comparision~~ Comparison of α1,2-mannosidase 1A, 1B, and 1C sequences: The DNA sequences of the three Class I α-1,2-mannosidases were analyzed to determine the amino acid coding sequence, including determination of the correct reading frame, identification of potential intron sequences, and identification of the correct translational start codon for each gene. A BLAST search of theα-1,2-mannosidase IA gene revealed two open reading frames (ORFs) separated by a region of DNA containing several stop codons which could indicate the presence of an intron sequence. To verify the presence of an intron at this site, PCR products spanning the putative intron were amplified from reverse-transcribed RNA (RT-PCR), cloned into vector and sequenced. Comparison of the α-mannosidase IA sequence with RT-PCR sequence verified the presence of a 50 bp intron at the expected splice junction. The intron contained a 5'-splice site (5'-GTAAGT-3') which matched the consensus sequence for filamentous fungi (5'-GTANGT-3'), and a 3'-splice site (5'-TAG-3') which matched the

consensus 5'-YAG-3' (Ballance, Transformation Systems for Filamentous Fungi and an Overview of Fungal Gene Structure, In Leong, S.A. and Berka, R.M. (eds.), *Molecular Industrial Mycology-Systems and Applications for Filamentous Fungi*, Dekker, Inc., New York, NY, pp. 1-29, 1991, 1986; Gurr et al., The Structure and Organization of Nuclear Genes of Filamentous Fungi, In Kinghorn (ed.), *Gene Structure in Eukaryotic Microbes*, IRL Press, Oxford, WA, pp. 93-139, 1987). The intron also contained an internal lariat sequence (5'-GCTGAC-3'; SEQ ID NO: 9), located 15 bp upstream of the 3'-splice site, consistent with the consensus 5'-(G/A)CT(G/A)AC-3'(SEQ ID NO: 19) for fungal introns.--

Please replace the paragraph on page 35, lines 23-31, with the following rewritten paragraph:

--The first potential translational start codon in the α-1,2-mannosidase 1B gene ~~occured~~ occurred 42 bp into the first ORF. Comparison of the coding region of this ORF with the *A. satoi* and *P. citrinum* α-1,2-mannosidase genes showed that the position of the putative translational start site correlated with the start sites of these genes. This start codon also contained a purine at the -3 position, a TATA-like element at position -76, and several CT-rich blocks in the sense strand. The first potential translational start codon of the α-mannosidase 1C gene occurred 38 bp into the ORF. The start site also contains a purine at position –3 and CCAAT motif at –221, but did not contain a clearly definable TATA box.--

Please replace the paragraph on page 37, lines 5-25, with the following rewritten paragraph:

--Mannosidase assays were performed using the disaccharide Man-α-1,2-Man-α-OCH_3 as a substrate in a coupled enzyme assay as described earlier (Scaman et al., *Glycobiol.* **6**:265-270, 1996), with some modifications. Digestion of the substrate was performed in a 30 μL final volume containing 27 μL of crude extract in 0.01M phosphate buffer (pH6.0) and 3 mL 100 mM disaccharide Man-α-1,2-Man-α-OCH_3 incubated at 37°C for 3 hours. Detection of released mannose was achieved by addition of 30 μL Tris-HCl (pH7.6) and 240 μL of ~~develping~~ developing solution, containing glucose oxidase (55 U/mL), horseradish peroxidase (1 U/mL) and o-dianisidine dihydrochloride (70 μg/mL), incubated at 37°C for 3 hours. Absorbance measurements at 450 nm determined final color change. Standard blanks included all components of the colrimetric reaction, plus the substrate. As a control, enzyme extracts which

were not used in the mannosidase digestion were subjected to the colorimetric reaction, to determine the absorbance which is due to the extract itself, and not due to mannose release. These values were subtracted from the absorbance values of the assays. Free mannose was used as a standard. All assays were performed in triplicate and the mean and standard deviation was calculated for each sample. Mannosidase activity was standardized by comparison with total protein in the crude enzyme extracts, and was defined as the amount of mannose released from substrate per μg of total protein per hour. Protein concentrations were determined by the Bradford method (Bradford, *Anal. Biochem.* **72**:248-254, 1976) using BSA as a standard.--